

AMENDMENTS

Please amend the currently pending claim set as follows:

1-74. (cancelled)

75. (currently amended) A method of determining the genotype of a subject at a locus within genetic material obtained from a biological sample from the subject, the method comprising:

- A. reacting the material at the locus to produce a first reaction value indicative of the presence of a given allele at the locus, wherein the first reaction value is the intensity of an allele-specific quantitative signal;
- B. forming a data set including the first reaction value;
- C. establishing a distribution set of probability distributions, including at least one distribution, associating hypothetical reaction value intensities with corresponding probabilities for each genotype of interest at the locus;
- D. applying the first reaction value to each pertinent probability distribution to determine a measure of the conditional probability of each genotype of interest at the locus, wherein the conditional probability is a measure of the likelihood of the genotype given the first reaction value; and
- E. determining the genotype of said subject based on the data obtained from step (D), wherein each allele is a single specific nucleotide.

76. (previously presented) A method according to claim 75, wherein the distribution set includes a plurality of probability distributions for a corresponding plurality of genotypes of interest.

77. (cancelled)

78. (previously presented) A method according to claim 76, further comprising:

- (i) reacting the material at the locus to produce a second reaction value;
- (ii) applying the first and second reaction values to each pertinent distribution to determine the probability of each genotype at the locus; and
- (iii) applying the first and second reaction values to each pertinent distribution to determine a measure of the conditional probability of each genotype at the locus.

79. (previously presented) A method according to claim 78, wherein each probability distribution associates a hypothetical pair of first and second reaction values with a single probability of each genotype of interest.

80. (previously presented) A method according to claim 75, wherein:
step (B) includes the step of including in the data set other reaction values obtained under conditions comparable to those under which the first reaction value was produced; and

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step (C) includes the step of using the reaction values in the data set to

establish the probability distributions;

the method further comprising:

performing steps (D) and (E) with respect to each of the reaction values.

81. (currently amended) A method, according to claim 80, of determining the genotype at a locus within genetic material obtained from each of a plurality of samples, the method further comprising:

- (i) performing step (A) with respect to the locus of material obtained from each sample; and
- (ii) in step (B), including in the data set reaction values obtained from each sample.

82. (currently amended) A method according to claim 80, of determining the genotype of selected loci within genetic material obtained from a sample, the method further comprising:

- (i) performing step (A) at each of the selected loci; and
- (ii) in step (B), including in the data set reaction values obtained from each of the selected loci.

83-84. (cancelled)

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85. (previously presented) A method according to claim 75, wherein step (E) further includes the step of calculating a confidence score, associated with the determination of the genotype in step (E), based on data from step (D).

86. (previously presented) A method according to claim 80, wherein step (E) further includes the step of calculating a confidence score, associated with the determination of the genotype in step (E), based on data from step (D), the method further comprising:

(F) determining whether a significant downward trend in confidence scores has occurred, and, in such event, entering an alarm condition.

87-90. (cancelled)

91. (previously presented) A method according to claim 78, wherein step (B) includes the step of including in the data set reaction values from prior tests at the locus obtained under comparable conditions.

92. (previously presented) A method according to claim 82, wherein the loci are selected on the basis of their ability to discriminate among subjects.

93. (canceled)

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94. (previously presented) A method according to claim 75, wherein step (A) includes the step of assaying for the given allele using genetic bit analysis, allele-specific hybridization, or allele-specific amplification, including such amplification by a polymerase chain reaction or a ligase chain reaction.

95. (previously presented) A method according to claim 82, wherein the loci are proximal to one another, so that the set of genotypes so produced may indicate a sequence of nucleotides associated with the genetic material.

96-115. (cancelled)

116. (new) A method of determining the genotype of a subject at a locus within genetic material obtained from a biological sample from the subject, the method comprising:

A. reacting the material at the locus to produce a first optical signal indicative of the presence of a first allele at the locus, wherein the first allele is a single specific nucleotide;

B. reacting the material at the locus to produce a second optical signal indicative of the presence of a second allele at the locus, wherein the second allele is a single specific nucleotide;

C. measuring the intensities of the first and second optical signals;

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D. establishing a probability distribution for each genotype of interest, wherein the probability distribution associates a hypothetical pair of optical signals with a corresponding measure of the probability of the genotype of interest and wherein the genotype of interest is either homozygous for the first allele, homozygous for the second allele, or heterozygous for the first and second alleles.

E. applying the pair of first and second measured intensities to each of the established probability distributions to determine a conditional probability of each genotype of interest at the locus; and

F. determining the genotype at the locus based on the data obtained from step (E).

117. (new) The method of claim 116 wherein step A includes the step of hybridizing a first oligonucleotide probe to the genetic material at the locus and step B includes the step of hybridizing a second oligonucleotide probe to the genetic material at the locus, wherein the first and second oligonucleotide probes are specific for the first and second alleles, respectively, at the locus.

118. (new) A method of determining the genotype of a diploid subject at a locus within genetic material obtained from a biological sample from the subject, the method comprising:

A. reacting the material at the locus to produce a first signal indicative of the presence of a first allele at the locus, wherein the first allele is a single specific nucleotide;

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- B. reacting the material at the locus to produce a second signal indicative of the presence of a second allele at the locus, wherein the second allele is a single specific nucleotide;
- C. measuring the intensities of the first and second signals;
- D. applying the pair of first and second signal intensities to a set of probability distributions associating hypothetical pairs of signal intensities with corresponding probabilities for each genotype of interest at the locus; and
- E. determining the genotype at the locus based on the data obtained from step D.